

Schreiber, David

131140

From: Schultz, James
Sent: Wednesday, August 25, 2004 5:16 PM
To: Schreiber, David
Subject: length over score search 09/925,139

Hi David,

I'm hoping to have this back by next wednesday (Sept. 1st, hopefully sooner!?)--could you let me know how realistic this is? Thanks for your help...

Doug

I need a length over score nucleotide sequence search on nucleotides 1631 to 1769 of SEQ ID NO:3 in the above entitled case. I need the lower and upper limits to be 8 and 50, respectively, I need any hits that are above 65% complementarity, and please transfer as many hits into the excel program as possible. Please do not search the interference databases at this time.

James Douglas Schultz, PhD

AU 1635 (Biotechnology)

Patent Examiner

United States Patent and Trademark Office

(Office) REM 2D18

(Mail) REM 2C18

(571) 272-0763

SEARCH REQUEST FORM**Scientific and Technical Information Center**

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>D. Schreiber</u>	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone #: <u>272-2526</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: <u>Rensselaer EOI A61</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr. Link _____
Date Completed: <u>8/30</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>13</u>	Fulltext _____	Sequence Systems <u>CompuLink</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>61</u>	Other _____	Other (specify) _____

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is _____.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.